

#7

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/612,809

DATE: 03/15/2002

TIME: 14:31:44

Input Set : A:\Iowa042.app

Output Set: N:\CRF3\03152002\I612809.raw

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MAR 25 2002
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3 <110> APPLICANT: SHEFFIELD et al., VAL C.
5 <120> TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR CONGENITAL HEART
6 DISEASE BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
8 <130> FILE REFERENCE: IOWA:042USD1
10 <140> CURRENT APPLICATION NUMBER: 09/612,809
11 <141> CURRENT FILING DATE: 2000-07-10
13 <160> NUMBER OF SEQ ID NOS: 2
15 <170> SOFTWARE: PatentIn Ver. 2.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 3946
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (475)..(2136)
26 <400> SEQUENCE: 1
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31 agtggtggca gaagggcgcc tgcttggtct ttctttttgt ctgctttccc ccgtttgcgc 180
33 ctggaagctg cgccgcgagt tcttgcaagg cggctctgcg cgcccgggcc cggccttctc 240
35 ccctgcgagc gacccgcctt cgccggccgc cgggccccga ggtagcccca ggcgcggag 300
37 gagccagccc cagcgcgcgc cgggagaggg ggcagcgcag ccggacgcac agcgcagcgg 360
39 gccggcacca gctcggcccg gcccggaact ggactcggcg gccggcgcg cgcggcccg 420
41 cccgagcgag ggtggggggc ggcgggcggc gcggggcggc ggcgagcggg ggcc atg 477
42 Met
43 1
45 caq gcg cgc tac tcc gtg tcc agc ccc aac tcc ctg gga gtg gtg ccc 525
46 Gln Ala Arg Tyr Ser Val Ser Ser Pro Asn Ser Leu Gly Val Val Pro
47 5 10 15
49 tac ctc ggc ggc gag cag agc tac tac cgc gcg gcg gcc gcg gcg gcc 573
50 Tyr Leu Gly Gly Glu Gln Ser Tyr Tyr Arg Ala Ala Ala Ala Ala
51 20 25 30
53 ggg ggc ggc tac acc gcc atg ccg gcc ccc atg agc gtg tac tcg cac 621
54 Gly Gly Gly Tyr Thr Ala Met Pro Ala Pro Met Ser Val Tyr Ser His
55 35 40 45
57 cct gcg cac gcc gag cag tac ccg ggc ggc atg gcc cgc gcc tac ggg 669
58 Pro Ala His Ala Glu Gln Tyr Pro Gly Gly Met Ala Arg Ala Tyr Gly
59 50 55 60 65
61 ccc tac acg ccg cag ccg cag ccc aag gac atg gtg aag ccg ccc tat 717
62 Pro Tyr Thr Pro Gln Pro Gln Pro Lys Asp Met Val Lys Pro Pro Tyr
63 70 75 80
65 agc tac atc gcg ctc atc acc atg gcc atc cag aac gcc ccg gac aag 765
66 Ser Tyr Ile Ala Leu Ile Thr Met Ala Ile Gln Asn Ala Pro Asp Lys

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67	85	90	95	
69 aag atc acc ctg aac ggc atc tac cag ttc atc atg gac cgc ttc ccc	813			
70 Lys Ile Thr Leu Asn Gly Ile Tyr Gln Phe Ile Met Asp Arg Phe Pro				
71 100 105 110				
73 ttc tac cgg gac aac aag cag ggc tgg cag aac agc atc cgc cac aac	861			
74 Phe Tyr Arg Asp Asn Lys Gln Gly Trp Gln Asn Ser Ile Arg His Asn				
75 115 120 125				
77 ctc tcg ctc aac gag tgc ttc gtc aag gtg ccg cgc gac gac aag aag	909			
78 Leu Ser Leu Asn Glu Cys Phe Val Lys Val Pro Arg Asp Asp Lys Lys				
79 130 135 140 145				
81 ccg ggc aag ggc agc tac tgg acg ctg gac ccg gac tcc tac aac atg	957			
82 Pro Gly Lys Gly Ser Tyr Trp Thr Leu Asp Pro Asp Ser Tyr Asn Met				
83 150 155 160				
85 ttc gag aac ggc agc ttc ctg cgg cgg cgg cgg cgc ttc aag aag aag	1005			
86 Phe Glu Asn Gly Ser Phe Leu Arg Arg Arg Arg Arg Phe Lys Lys Lys				
87 165 170 175				
89 gac gcg gtg aag gac aag gag gag aag gac agg ctg cac ctc aag gag	1053			
90 Asp Ala Val Lys Asp Lys Glu Glu Lys Asp Arg Leu His Leu Lys Glu				
91 180 185 190				
93 ccg ccc ccg ccc ggc cgc cag ccc ccg ccc gcg ccg ccg gag cag gcc	1101			
94 Pro Pro Pro Pro Gly Arg Gln Pro Pro Pro Ala Pro Pro Glu Gln Ala				
95 195 200 205				
97 gac ggc aac gcg ccc ggt ccg cag ccg ccg ccc gtg cgc atc cag gac	1149			
98 Asp Gly Asn Ala Pro Gly Pro Gln Pro Pro Pro Val Arg Ile Gln Asp				
99 210 215 220 225				
101 atc aag acc gag aac ggt acg tgc ccc tcg ccg ccc cag ccc ctg tcc	1197			
102 Ile Lys Thr Glu Asn Gly Thr Cys Pro Ser Pro Pro Gln Pro Leu Ser				
103 230 235 240				
105 ccg gcc gcc gcc ctg ggc agc ggc agc gcc gcc gcg gtg ccc aag atc	1245			
106 Pro Ala Ala Ala Leu Gly Ser Gly Ser Ala Ala Ala Val Pro Lys Ile				
107 245 250 255				
109 gag agc ccc gac agc agc agc agc agc ctg tcc agc ggg agc agc ccc	1293			
110 Glu Ser Pro Asp Ser Ser Ser Ser Ser Leu Ser Ser Gly Ser Ser Pro				
111 260 265 270				
113 ccg ggc agc ctg ccg tcg gcg cgg ccg ctc agc ctg gac ggt gcg gat	1341			
114 Pro Gly Ser Leu Pro Ser Ala Arg Pro Leu Ser Leu Asp Gly Ala Asp				
115 275 280 285				
117 tcc gcg ccg ccg ccg ccc gcg ccc tcc gcc ccg ccg ccg cac cat agc	1389			
118 Ser Ala Pro Pro Pro Pro Ala Pro Ser Ala Pro Pro Pro His His Ser				
119 290 295 300 305				
121 cag ggc ttc agc gtg gac aac atc atg acg tcg ctg ccg ggg tcg ccg	1437			
122 Gln Gly Phe Ser Val Asp Asn Ile Met Thr Ser Leu Arg Gly Ser Pro				
123 310 315 320				
125 cag agc gcg gcc gcg gag ctc agc tcc ggc ctt ctg gcc tcg gcg gcc	1485			
126 Gln Ser Ala Ala Glu Leu Ser Ser Gly Leu Leu Ala Ser Ala Ala				
127 325 330 335				
129 gcg tcc tcg cgc gcg ggg atc gca ccc ccg ctg gcg ctc ggc gcc tac	1533			
130 Ala Ser Ser Arg Ala Gly Ile Ala Pro Pro Leu Ala Leu Gly Ala Tyr				
131 340 345 350				

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133 tcg ccc ggc cag agc tcc ctc tac agc tcc ccc tgc agc cag acc tcc 1581
134 Ser Pro Gly Gln Ser Ser Leu Tyr Ser Ser Pro Cys Ser Gln Thr Ser
135 355 360 365
137 agc gcg ggc agc tcg ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc 1629
138 Ser Ala Gly Ser Ser Gly Gly Gly Gly Gly Ala Gly Ala Ala Gly
139 370 375 380 385
141 ggc gcg ggc ggc gcc ggc acc tac cac tgc aac ctg caa gcc atg agc 1677
142 Gly Ala Gly Gly Ala Gly Thr Tyr His Cys Asn Leu Gln Ala Met Ser
143 390 395 400
145 ctg tac gcg gcc ggc gag cgc ggc ggc cac ttg cag ggc gcg ccc ggc 1725
146 Leu Tyr Ala Ala Gly Glu Arg Gly Gly His Leu Gln Gly Ala Pro Gly
147 405 410 415
149 ggc gcg ggc ggc tcg gcc gtg gac aac ccc ctg ccc gac tac tct ctg 1773
150 Gly Ala Gly Gly Ser Ala Val Asp Asn Pro Leu Pro Asp Tyr Ser Leu
151 420 425 430
153 cct ccg gtc acc agc agc agc tcg tcg tcc ctg agt cac ggc ggc ggc 1821
154 Pro Pro Val Thr Ser Ser Ser Ser Ser Ser Ser Leu Ser His Gly Gly Gly
155 435 440 445
157 ggc ggc ggc ggc ggc ggc gag gag gcc ggc cac cac cct gcg gcc 1869
158 Gly Gly Gly Gly Gly Gly Gln Glu Ala Gly His His Pro Ala Ala
159 450 455 460 465
161 cac caa ggc cgc ctc acc tcg tgg tac ctg aac cag gcg ggc gga gac 1917
162 His Gln Gly Arg Leu Thr Ser Trp Tyr Leu Asn Gln Ala Gly Gly Asp
163 470 475 480
165 ctg ggc cac ttg gca agc gcg gcg gcg gcg gcg gcg gcc gca ggc tac 1965
166 Leu Gly His Leu Ala Ser Ala Ala Ala Ala Ala Ala Ala Gly Tyr
167 485 490 495
169 ccg ggc cag cag cag aac ttc cac tcg gtg cgg gag atg ttc gag tca 2013
170 Pro Gly Gln Gln Gln Asn Phe His Ser Val Arg Glu Met Phe Glu Ser
171 500 505 510
173 cag agg atc ggc ttg aac aac tct cca gtg aac ggc aat agt agc tgt 2061
174 Gln Arg Ile Gly Leu Asn Asn Ser Pro Val Asn Gly Asn Ser Ser Cys
175 515 520 525
177 caa atg gcc ttc cct tcc agc cag tct ctg tac cgc acg tcc gga gct 2109
178 Gln Met Ala Phe Pro Ser Ser Gln Ser Leu Tyr Arg Thr Ser Gly Ala
179 530 535 540 545
181 ttc gtc tac gac tgt agc aag ttt tga cacaccctca aagccgaact 2156
182 Phe Val Tyr Asp Cys Ser Lys Phe
183 550
185 aaatcgaacc ccaaaagcagg aaaagctaaa ggaacccatc aaggcaaaat cgaaactaaa 2216
187 aaaaaaaaaat ccaattaaaaa aaaacccctg agaatatcca ccacaccagc gaacagaata 2276
189 tccctccaaa aattcagctc accagcacca gcaagagaa aactctattt tcttaaccga 2336
191 ttaattcaga gccacctcca ctttgccctg tctaaataaa caaacccgta aactgtttta 2396
193 tacagagaca gcaaaatcctt ggtttattaa aggacagtgt tactccagat aacacgtaag 2456
195 tttcttcttg cttttcagag acctgcttcc cctctctccc gtctcccttc tcttgcttc 2516
197 ttccttgcc ctcacctgta agatattatt ttatctatg ttgaaggag ggggaaagtc 2576
199 cccgtttatg aaagtcgctt tctttttatt catggacttg ttttaaaatg taaattgcaa 2636
201 catagtaatt tatttttaatt ttgtagttgg atgtcgtgga ccaaagccca gaaagtgttc 2696
203 ccaaaacctg acgttaaaatt gctgaaact ttaattgtg ctttttttct cattataaaa 2756

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205 agggaaactg tattaatctt attctatcct cttttctttc tttttgttga acatattcat 2816
207 tgtttgttta ttaataaaatt accattcagt ttgaatgaga cctatatgtc tggatacttt 2876
209 aatagagctt taattattac gaaaaaagat ttcagagata aaacactaga agttacctat 2936
211 tctccaccta aatctctgaa aaatggagaa accctctgac tagtccatgt caaatttttac 2996
213 taaaagtctt tttgtttaga tttattttcc tgcagcatct tctgcaaaat gtactatata 3056
215 gtcagcttgc tttgaggcta gtaaaaagat atttttctaa acagattgga gttggcatat 3116
217 aaacaaatac gttttctcac taatgacagt ccatgattcg gaaattttaa gcccatgaat 3176
219 cagccgcggt cttaccacggt tgatgcctgt gtgccgagag atgggactgt gcggccagat 3236
221 atgcacagat aaatatttgg cttgtgtatt ccatataaaa ttgcagtgc a tattatacat 3296
223 cctgttgagc cagatgctga atagattttt tctattattt tcagtccttt ataaaaaggaa 3356
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229 ttgagaaact attttagaaa atatgtttgt agaacaatta tttttgaaaa agatttaaag 3536
231 caataacaag aaggaaggcg agaggagcag aacattttgg tctagggtgg tttcttttta 3596
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235 ccttttgtaa ataaccacgg aaatgtaata aattcattat cttagggtga tctgccctgc 3716
237 caatcagact ttggggagat ggcgatttga ttacagacgt tccgggggggt ggggggcttg 3776
239 cagtttgttt tggagataat acagtttctt gctatctgcc gctcctatct agaggcaaca 3836
241 cttaagcagt aattgctggt gcttggtgtc aaaatttgat cattgtttaa ggattgctgc 3896
243 aaataaatac actttaattt cagtcaaaaa aaaaaaaaaa aaaaaaaaaa 3946

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246 <210> SEQ ID NO: 2

247 <211> LENGTH: 553

248 <212> TYPE: PRT

249 <213> ORGANISM: Homo sapiens

251 <400> SEQUENCE: 2

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255             20             25             30
256 Ala Gly Gly Gly Tyr Thr Ala Met Pro Ala Pro Met Ser Val Tyr Ser
257             35             40             45
258 His Pro Ala His Ala Glu Gln Tyr Pro Gly Gly Met Ala Arg Ala Tyr
259             50             55             60
260 Gly Pro Tyr Thr Pro Gln Pro Gln Pro Lys Asp Met Val Lys Pro Pro
261             65             70             75             80
262 Tyr Ser Tyr Ile Ala Leu Ile Thr Met Ala Ile Gln Asn Ala Pro Asp
263             85             90             95
264 Lys Lys Ile Thr Leu Asn Gly Ile Tyr Gln Phe Ile Met Asp Arg Phe
265             100            105            110
266 Pro Phe Tyr Arg Asp Asn Lys Gln Gly Trp Gln Asn Ser Ile Arg His
267             115            120            125
268 Asn Leu Ser Leu Asn Glu Cys Phe Val Lys Val Pro Arg Asp Asp Lys
269             130            135            140
270 Lys Pro Gly Lys Gly Ser Tyr Trp Thr Leu Asp Pro Asp Ser Tyr Asn
271             145            150            155            160
272 Met Phe Glu Asn Gly Ser Phe Leu Arg Arg Arg Arg Phe Lys Lys
273             165            170            175
274 Lys Asp Ala Val Lys Asp Lys Glu Glu Lys Asp Arg Leu His Leu Lys
275             180            185            190

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276 Glu Pro Pro Pro Pro Gly Arg Gln Pro Pro Pro Ala Pro Pro Glu Gln
277      195      200      205
278 Ala Asp Gly Asn Ala Pro Gly Pro Gln Pro Pro Pro Val Arg Ile Gln
279      210      215      220
280 Asp Ile Lys Thr Glu Asn Gly Thr Cys Pro Ser Pro Pro Gln Pro Leu
281 225      230      235      240
282 Ser Pro Ala Ala Ala Leu Gly Ser Gly Ser Ala Ala Ala Val Pro Lys
283      245      250      255
284 Ile Glu Ser Pro Asp Ser Ser Ser Ser Ser Leu Ser Ser Gly Ser Ser
285      260      265      270
286 Pro Pro Gly Ser Leu Pro Ser Ala Arg Pro Leu Ser Leu Asp Gly Ala
287      275      280      285
288 Asp Ser Ala Pro Pro Pro Pro Ala Pro Ser Ala Pro Pro Pro His His
289      290      295      300
290 Ser Gln Gly Phe Ser Val Asp Asn Ile Met Thr Ser Leu Arg Gly Ser
291 305      310      315      320
292 Pro Gln Ser Ala Ala Ala Glu Leu Ser Ser Gly Leu Leu Ala Ser Ala
293      325      330      335
294 Ala Ala Ser Ser Arg Ala Gly Ile Ala Pro Pro Leu Ala Leu Gly Ala
295      340      345      350
296 Tyr Ser Pro Gly Gln Ser Ser Leu Tyr Ser Ser Pro Cys Ser Gln Thr
297      355      360      365
298 Ser Ser Ala Gly Ser Ser Gly Gly Gly Gly Gly Gly Ala Gly Ala Ala
299      370      375      380
300 Gly Gly Ala Gly Gly Ala Gly Thr Tyr His Cys Asn Leu Gln Ala Met
301 385      390      395      400
302 Ser Leu Tyr Ala Ala Gly Glu Arg Gly Gly His Leu Gln Gly Ala Pro
303      405      410      415
304 Gly Gly Ala Gly Gly Ser Ala Val Asp Asn Pro Leu Pro Asp Tyr Ser
305      420      425      430
306 Leu Pro Pro Val Thr Ser Ser Ser Ser Ser Ser Leu Ser His Gly Gly
307      435      440      445
308 Gly Gly Gly Gly Gly Gly Gly Gln Glu Ala Gly His His Pro Ala
309      450      455      460
310 Ala His Gln Gly Arg Leu Thr Ser Trp Tyr Leu Asn Gln Ala Gly Gly
311 465      470      475      480
312 Asp Leu Gly His Leu Ala Ser Ala Ala Ala Ala Ala Ala Ala Gly
313      485      490      495
314 Tyr Pro Gly Gln Gln Gln Asn Phe His Ser Val Arg Glu Met Phe Glu
315      500      505      510
316 Ser Gln Arg Ile Gly Leu Asn Asn Ser Pro Val Asn Gly Asn Ser Ser
317      515      520      525
318 Cys Gln Met Ala Phe Pro Ser Ser Gln Ser Leu Tyr Arg Thr Ser Gly
319      530      535      540
320 Ala Phe Val Tyr Asp Cys Ser Lys Phe
321 545      550

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VERIFICATION SUMMARY

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